

# FIG. 1A

10	CCTGAAGGGAGGCCAGGAGAGAGGACACTGGCCAGAGAGGGCTCTGGGCACTGGAGG	50
70	GACGGCTCTTCTCTGCCAGGGGTCCCTGGCCGATGGGATCACGCAGAAGAAATGCCAG	110
130	AGAAGGCAGCCTTTGAGAAGGGAAAGTCACTATCCAGAGCCCAGACTGAGGGGATGGAGCTT	170
		M E L
190	GAGGAAGTACGGCCCTGGAAAGAACTGGGGACAGTTATAGGAGGGAGCTGCTCAGAGTAA	210
R K Y G P G R L A G T V I G G A A Q S K	250	290
S Q T K S D S I T K E F L P G L Y T A P	310	350
ATCACAGACTAAATCAGACTCAATCACAAAGAGTTCCCTGCCAGGGCTTACACAGCCCC	390	410
S S P F P P S Q V S D H Q V L N D A E V	430	470
TGCGCCCTCCTGGAGAACTTCAGCTCTCCTATGACTATGGAGAAACCGAGAGTGA	490	530
A A L L E N F S S Y D Y G E N E S D S		
GTGCTGTACCTCCGCCCTGGCCACAGGACTTCAGCCTGAACCTTCGACCCCTTCCT		
C C T S P P C P Q D F S L N F D R A F L		

MATCH WITH FIG. 1B

B  
C  
D

## WATCH WITH FIG. 1A

## MATCH WITH FIG. 11C

## MATCH WITH FIG. 1B

## FIG. 1C

970	990	1010
GGTGCTGCAGCTGGCTGGCTGGCTTCTGCCCTGCTGGTCATGGCTACTGCTATGCGC		
V L Q L V A G F L L P L L V M A Y C Y A		
1030	1050	1070
CCACATCCTGGCCGGTGGCTGGCTGGTTCCAGGGGCCAGGGCCCTGGGGCCATGGGGCT		
H I L A V L L V S R G Q R R L R A M R L		
1090	1110	1130
GGTGGCTGGCTGGCTGGCCTTGGCTGGCCCTCTGGACCCCCCTATCACCTGGTGGCTGCT		
V V V V V A F A L C W T P Y H L V V L		
1150	1170	1190
GGTGGACATCCTCATGGACCTGGGGCTTGGGGCAACTGTTGGCCGAGAAAGCAGGGT		
V D I L M D L G A A L A R N C G R E S R V		
1210	1230	1250
AGACGTGGCCAAGTCGGTCACCTCAGGCCCTGGCTACATGCCACTGCTGGCTAACCCGCT		
D V A K S V T S G L G Y M H C C L N P L		
1270	1290	1310
GCTCTATGCCATTGTAGGGCTCAAGTCCGGAGGGATGTGGATGCTTGTGGCT		
L Y A F V G V K F R E R M W M L L R L		

## MATCH WITH FIG. 1D

## MATCH WITH FIG. 1C

卷之三

1330 1350 1370  
 GGGCTGCCCAACCAAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCCGGGATTCATC  
 G C P N Q R G L Q R Q P S S R R D S S  
 1390 1410 1430  
 CTGGCTCTGAGACCTCAGAGGCCTACTCGGGCTTGTGAGGGCGGAATCCGGCTCCCC  
 W S E T S E A S Y S G L \* 1450 1470 1490  
 TTTGGCCACAGTCTGACTTCCCCGATTCCAGGCTTCCCTCCCTCTGCCGGCTCTGG  
 1510 1530 1550  
 CTCTCCCCAATATCCCTCGCTCCGGGACTCACTGGCAGCCCCAGCACCCAGGTCTCCC  
 1570 1590 1610  
 GGAAGCCACCCCTCCAGCTCTGAGGAAGTCGCACCATTGCTGCTCCCTAGCTGCCAAGCCC  
 1630 1650 1670  
 CATCCTGCCGGCGAGGTGGCTGCCCTGGAGCCCCACTGCCCTCTCATTTGGAAACTAAA  
 1690 1710 1730  
 ACTTCATCTCCCCAAGTGGGGAGTACAAGGCATGGCGTAGAGGGTAGCTGCCCATGA  
 1750 1770 1790  
 AGCCACAGCCCCAGGCCCTCCAGCTCAGCAGTGAAGTGGCCATGGTGGCTCATGGTCCCCAAGACCTCTAT  
 1810 1830 1850  
 ATTTGGTCTTTTATTGTCTAAATCCTGCTAAAACCTTTCAATAAACAGATCG  
 1870  
 TCAGGAAAAAA

5 / 6

## F | G. 2A

54	DHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFL	103
2	ESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPE . . .	SLEINKYFV 46
104	PAL <del>X</del> SLLFILLGLLNGAVAAVLLSRRTALSSTDTFLLLAVADTLVLTL	153
47	VIIYALVFLLSLLGNLSLVMVILYSRVGRSVTDVYLLNLALLFALT	96
154	PLWAVDAAVQWVFGSGLCKVAGALEFNINFYAGALLACISFDRYLNIVHA	203
97	PIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLACISVDRYLAIVHA	146
204	TQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYN	253
147	TRTLTO.KRYLVKFICLSSIWGLSLLALPVLLFRRTVYSSNNVSPACYEDM	195
254	FPQVG..RTALRVILQLVAGFLLPLLVMAWCYAHILAVLLVSRGQRRLLRAM	301
196	GNNTANWRMLLRLPQSFQFIVPLLIMLFCYGFTRLTFKAHMGQKHRAM	245

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

F | G. 2B

6 / 6

302 RLVVVVVVVAFAFCWTPYHILVVLVDILMDLGALARNCGRESRVDVAKSVTS 351

246 RVIFAVVLFLLCWL PYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 295

352 GLGYMHCCLNPLLYAFVGVKFERMMWMLLRLGGCPNQRGQLQRQPSSSRRD 401

296 ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVG 345

402 SSWSETSEA 410

346 SSSGHTSTT 354



VIA HAND DELIVERY MARCH 18, 2002

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

**SUBMISSION OF SUBSTITUTE FORMAL DRAWINGS**

Commissioner for Patents  
Washington, D.C. 20231

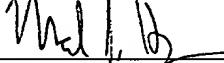
To the Official Draftsperson:

Applicants submit herewith Substitute Formal Drawings of Figures 1A-1D and 2A-2B (six sheets) to replace the previously filed drawings of Figures 1A-1D and 2A-2B (six sheets). The enclosed drawings have been amended to correspond to the sequences shown in the Substitute Sequence Listing filed herewith, as discussed in detail in the Response and Amendment also filed herewith.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: March 18, 2002

  
\_\_\_\_\_  
Mark J. Hyman (Reg. No. 46,789)  
Attorney for Applicants

**Human Genome Sciences, Inc.**  
9410 Key West Avenue  
Rockville, MD 20850  
(240) 314-1224

Enclosures  
KKH/MJH/KC/mlm

# FIG. 1A

10 CCTGAAAGGGAGGAGGCAGGGAGAGAGGACAGTGGCCAGAGGGCTCTGGGCACGGAGG  
30 50  
70 GACGCTCTTCTGCCAGGGGTCCCTGGGCCATGGATCACGCAGAAAGAATGCGAG  
90 110  
130 150 170  
190 210 230  
R K Y G P G R L A G T V I G G A A Q S K  
250 270 290  
S Q T K S D S I T K E F L P G L Y T A P  
310 330 350  
ATCACAGACTAAATCAGACTCAATCACAAAGAGTTCCAGGCCCTTACACAGCCCC  
370 390 410  
TTCCCTCCCGTTCCCGCCCTCACAGGTGAGTGACCAAGTGCTAAATGACGCCGAGGT  
S S P F P P S Q V S D H Q V L N D A E V  
430 450 470  
TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCATTGACTATGGAGAAAACGAGAGTGACTC  
A A L L E N F S S S Y D Y G E N E S D S  
C C T S P P C P Q D F S L N F D R A F L

**FIG. 1B**

**FIG. 1C**

910	GGGCCTAACGCCACCCACTGCCAATAACA	ACTTCCCACAGGTGGCCGGCACGGCTCTGCG	930	950															
R	L	N	A	T	H	C	Q	Y	N	F	P	Q	V	G	R	T	A	L	R
970	GGTGCTGCAGCTGGCTGGCTTCTGCCCTGCTGGCTACTGGCTACTGCTATGC	990	1010																
V	L	Q	L	V	A	G	F	L	L	P	L	L	V	M	A	Y	C	Y	A
1030	CCACATCCTGGCCCGTGGCTGGTTCCAGGGGCCAGGGGCCAGGGCCATGGGCT	1050	1070																
H	I	L	A	V	L	V	S	R	G	Q	R	R	L	R	A	M	R	L	
1090	GGTGGTGGTGGTGGCTGGCTGGCCCTTGGACCCCCCTATCACCTGGTGGT	1110	1130																
V	V	V	V	A	F	A	L	C	W	T	P	Y	H	L	V	V	L		
1150	GGTGGACATCCTCATGGACCTGGCGCTTGGCCGGCAACTGTGGCCGAGAAAGCAGG	1170	1190																
V	D	I	L	M	D	L	G	A	L	A	R	N	C	G	R	E	S	R	V
1210	AGACGTTGCCAAGTCGGTCAACCTCAGGCCCTGGGCTACATGCCACTGCTGCCAACCCGCT	1230	1250																
D	V	A	K	S	V	T	S	G	L	G	Y	M	H	C	C	L	N	P	L
1270	GCTCTATGCCCTTGTAGGGTCAAGTTCCGGGAGTCGGATGTGGATGCTCTTGC	1290	1310																
H	Y	A	F	V	G	V	K	F	R	E	R	M	W	M	L	R	L		

FIG. 1D

1330	GGGCTGCCCAACCAGAGGGCTCCAGGGCAGGGCATCGTCTTCCGGGGATTCATC	1350		1370
G C P N Q R G L Q R Q P S S R R D S S				
1390	CTGGTCTGAGACCTCAGGGCCTCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCC	1410		1430
W S E T S E A S Y S G L *				
1450	TTTCGCCACAGTCTGACTTCCCGCATTCAGGCTCCCTCCAGGGTCTCTGG	1470		1490
1510	CTCTCCCCAATATCCTCGCTCCGGACTCACTGGCAGCCCCAGCACCCAGGTCTCCC	1530		1550
1570	GGGAAGCCACCCCTCCCAAGCTCTGAGGACTGCACCATTGCTCCCTAGCTGCCAAGGCC	1590		1610
1630	CATCCTGCCGCCCGAGGTGGCTGCCACTGGAGCCCCACTGCCCTCTCATTTGAAACTAAA	1650		1670
1690	ACTTCATCTCCCCAAGTGGGGAGTACAAGGCATGGCTAGGGTAGCTGCCCATGA	1710		1730
1750		1770		1790
1810	AGCCACAGGCCAGGGCTCCAGCTCAGCAGTGAATGGCCATGGTCCCCAAGACCTCTAT	1830		1850
1870	ATTGGTCTTTATTGTCTAAACTTCTGCTTAAATCCCTCAATAAACAAAGATCG			
	TCAGGGAAAAAA			

FIG. 2 A

54	DHQVLNDAEVAVALLENFSSSYDGENESDSCCTSPPCPQDFSLNFDR AFL	103
2	ESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPE...	46
104	PALYSLLFILLGNGAVAVLLSRRTALSSSTDTFILLHLAVADTILLVLT	153
47	VITIYALVFLLSLLGNSLVMVILYSRVGRSVTDVYILLALADLIFALT	96
1154	PLWAVDAAVQWVFGSSGLCKVAGALENNINFYAGALLACISFDRLNIVHA	203
97	PIWAASKVNGWIFGTFLCKVVSLLKEVNIFYSGILLACISVDRLAI VHA	146
2204	TQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYN	253
147	TRTLTQ.KRYLVKFICLSIWGGLSLLLALPVLLFRRTVSSNVSPACYEDM	195
2254	FPQVG.RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLLRAM	301
196	GNNTANWRMLLRILPQSFGFIVPPLLIMLFCYGFTLRTLFKAHMGOKH RAM	245

FIG. 2 B

302	RLVvvvvvAFALCWTPTYHLLVVLVDILMMDLGALARNCGRESRVDVAKSVTS	351
246	RVIFAVVLLIFLLCWLWPYNLVLLADTLMRTQVVIQETCERRNHIDRALDATE	295
352	GLGYMHCCLNPLLLYAFVGVKFRERMWMLLRLGCPNQRGQLQRQPSSRRD	401
296	ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVG	345
402	SSWSETSEA	410
346	SSSSGHTSTTT	354

VIA HAND DELIVERY MARCH 18, 2002

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li Attorney Docket No.: PF218US  
Application Serial No.: 09/101,518 Art Unit: 1646  
Filed: January 11, 1996 Examiner: Pak, M.  
Title: Human G-Protein Chemokine Receptor HSATU68

**STATEMENT UNDER 37 C.F.R. §§1.821 AND 1.825**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Pursuant to 37 C.F.R. §§1.821(f) and 1.825(b), Applicants hereby certify that the sequence listing information recorded in computer readable form and submitted herewith is identical to the written (on paper) Substitute Sequence Listing submitted herewith.

Applicants further certify under 37 C.F.R. §§1.821(g) and 1.825(a) that the Substitute Sequence Listing submitted herewith contains no new matter.

Respectfully submitted,

Dated: March 18, 2002

Mark J. Hyman  
Attorney for Applicants

Reg. No. 46,789

**Human Genome Sciences, Inc.**  
9410 Key West Avenue  
Rockville, MD 20850  
Telephone: (240) 314-1224

Enclosures  
KKH/MJH/KC

---

SEQUENCE LISTING

<110> Li, Yi

<120> Human G-Protein Chemokine Receptor HSATU68

<130> PF218US

<140> US 09/101,518

<141> 1998-12-21

<150> PCT/US96/00499

<151> 1996-01-11

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 1876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (173)..(1420)

<223>

*Y2*

<400> 1

cctgaaggga gagcagggag agagaggaca gtggccagag aggctctgg gcactggagg 60

gacgctcttc ttccctgcccc ggggtccctg ggccgatggg atcacgcaga agaatgcgag 120

agaagcagcc tttgagaagg gaagtcacta tcccagagcc cagactgagc gg atg gag 178

Met Glu  
1

ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga 226

Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly  
5 10 15

gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag 274

Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu  
20 25 30

ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca 322

Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser  
35 40 45 50

cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc 370

Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu  
55 60 65

ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac 418

Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp  
70 75 80

tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc 466  
 Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe  
 85 90 95

gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt ctg ctg ggg 514  
 Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu Leu Gly  
 100 105 110

ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc cgg cgg aca 562  
 Leu Leu Gly Asn Gly Ala Val Ala Val Leu Leu Ser Arg Arg Thr  
 115 120 125 130

gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct gta gca gac 610  
 Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val Ala Asp  
 135 140 145

acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac gct gcc gtc 658  
 Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala Ala Val  
 150 155 160

cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt gcc ctc ttc 706  
 Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala Leu Phe  
 165 170 175

aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc atc agc ttt 754  
 Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile Ser Phe  
 180 185 190

gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac cgc cgg ggg 802  
 Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg Arg Gly  
 195 200 205 210

ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg ggg ctc tgc 850  
 Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly Leu Cys  
 215 220 225

ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tgc gcc cac cac gac 898  
 Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His His Asp  
 230 235 240

gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca cag gtg ggc 946  
 Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln Val Gly  
 245 250 255

cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt ctg ctg ccc 994  
 Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu Leu Pro  
 260 265 270

ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc gtg ctg ctg 1042  
 Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val Leu Leu  
 275 280 285 290

gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg gtg gtg gtg 1090  
 Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val Val Val  
 295 300 305

gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac ctg gtg gtg 1138  
 Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu Val Val  
 310 315 320

ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc 1186  
 Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly  
 325 330 335

cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc 1234  
 Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly  
 340 345 350

tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc 1282  
 Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val  
 355 360 365 370

aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc 1330  
 Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro  
 375 380 385

aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca 1378  
 Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Arg Arg Asp Ser  
 390 395 400

tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga 1420  
 Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu  
 405 410 415

ggccggaatc cgggctcccc tttcgccac agtctgactt ccccgattc caggctcctc 1480  
 cctccctctg ccggctctgg ctctcccaa tattcctcgct cccggactc actggcagcc 1540  
 ccagcaccac caggtctccc gggaaagccac cctcccaagct ctgaggactg caccattgt 1600  
 gctccttagc tgccaagccc catcctgccc cccgaggtgg ctgcctggag ccccactgcc 1660  
 cttctcattt ggaaactaaa acttcatctt ccccaagtgc gggaggtaca aggcatggcg 1720  
 tagagggtgc tgccccatga agccacagcc caggcctcca gtcagcagt gactgtggcc 1780  
 atggtccccca agacctctat atttggtctt ttattttat gtctaaaatc ctgcttaaaa 1840  
 cttttcaata aacaagatcg tcaggaaaaaa aaaaaa 1876

<210> 2  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Glu Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile  
 1 5 10 15

Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr  
 20 25 30

Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro  
 35 40 45

Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala

50

55

60

Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu

65

70

75

80

Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu

85

90

95

Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu

100

105

110

Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg

115

120

125

Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val

130

135

140

Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala

145

150

155

160

Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala

165

170

175

Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile

180

185

190

Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg

195

200

205

Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly

210

215

220

Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His

225

230

235

240

His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln

245

250

255

Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu

260

265

270

Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val

275

280

285

Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val  
290 295 300

Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu  
305 310 315 320

Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn  
325 330 335

Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly  
340 345 350

Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val  
355 360 365

Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly  
370 375 380

Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg  
385 390 395 400

Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu  
405 410 415

<210> 3

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Contains a BamHI restriction enzyme site

<400> 3

cgggatccctc catggagttg aggaagttac

29

<210> 4

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Contains complementary sequences to a BamHI site

<400> 4

ggcggatccc gctcacaaggc ccgagtagga

30

<210> 5

<211> 34

<212> DNA

<213> Artificial sequence

<220>  
 <223> Contains a HindIII site  
  
 <400> 5  
 gtc caa gctt gcc accatgg agtt gagaa gtac 34

<210> 6  
 <211> 57  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains complementary sequences to a XhoI site, translation stop codon, and an HA tag

<400> 6  
 ctg ctcgagt caagcgtagt ctgggacgtc gtatggtag cacaagcccg agtagga 57

<210> 7  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains a BamHI restriction enzyme site followed by 5 nucleotides resembling an efficient signal for the initiation of translation in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M. .)

<400> 7  
 cgg gatcc ct ccatggagt tgaggaagta c 31

<210> 8  
 <211> 29  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains the cleavage site for the restriction endonuclease BamHI

<400> 8  
 cgg gatcc cg ctcacaagcc cgagtagga 29

<210> 9  
 <211> 353  
 <212> PRT  
 <213> Homo sapiens

<400> 9

Glu	Ser	Asp	Ser	Phe	Glu	Asp	Phe	Trp	Lys	Gly	Glu	Asp	Leu	Ser	Asn
1				5				10					15		

Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro  
20 25 30

Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile  
35 40 45

Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met  
50 55 60

Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr  
65 70 75 80

Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro  
85 90 95

Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu  
100 105 110

Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile  
115 120 125

*D2*  
*cont.*  
Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His  
130 135 140

Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile Cys  
145 150 155 160

Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu Leu  
165 170 175

Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr Glu  
180 185 190

Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile Leu  
195 200 205

Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe Cys  
210 215 220

Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys  
225 230 235 240

His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu  
245 250 255

Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg  
260 265 270

Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp Arg  
275 280 285.

Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu Asn  
290 295 300

Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu Leu  
305 310 315 320

Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro Lys  
325 330 335

Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser Thr  
340 345 350

Thr

*D<sup>2</sup>*  
*cont.*

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Li

Attorney Docket No.: PF218US

Application Serial No.: 09/101,518

Art Unit: 1646

Filed: January 11, 1996

Examiner: Pak, M.

Title: Human G-Protein Chemokine Receptor HSATU68

**DECLARATION OF MELANIE LENHART UNDER 37 C.F.R. § 1.132**

I, Melanie Lenhart, hereby declare and state as follows:

1. I am employed by Human Genome Sciences, Inc. ("HGS"), Rockville, Maryland, as a Manager in the PreClinical Discovery department. Since I began working at HGS in 1995, my duties have primarily included carrying out and analyzing, as both a bench scientist and a manager, extensive DNA sequencing.

2. A partially redacted copy of the American Type Culture Collection ("ATCC") deposit receipt for Deposit Number 97334 is attached hereto as Exhibit A. As the deposit receipt indicates, ATCC Deposit Number 97334 contains a DNA plasmid assigned to the HGS Code Number 498,333, also known within HGS as HGS Clone ID HSATU68. I requested from the ATCC a sample of ATCC Deposit Number 97334 by a purchase order numbered 81449 dated March 13, 2001, a copy of which is attached hereto as Exhibit B. I received the sample of ATCC Deposit Number 97334 from the ATCC in April of 2001, as evidenced by Sales Order # S0241638 from the ATCC, a copy of which is attached hereto as Exhibit C.

3. I have been shown what has been presented to me as Figures 1A-1D as originally filed in the above-captioned patent application (hereinafter "original Figures

1A-1D"), a copy of which original Figures 1A-1D is attached hereto as Exhibit D. I used the nucleotide sequence of HSATU68, as shown in original Figures 1A-1D, as a reference to compare to the nucleotide sequence of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334.

4. A sample of ATCC Deposit Number 97334 was thoroughly sequenced under my supervision in my laboratory at HGS using sequencing methods which were routine and well known in the art prior to January 11, 1996. Exhibit E depicts an alignment of the nucleotide sequence of the deposited clone with the nucleotide sequence shown in original Figures 1A-1D.

5. The nucleotide sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at position 491. More particularly, original Figures 1A-1D show an A residue at position 491, while a T residue is present in the sequence obtained from the DNA clone contained in ATCC Deposit Number 97334.

6. As a result of the above difference at position 491 of the nucleotide sequence, the encoded amino acid sequence shown in original Figures 1A-1D differs from the sequence obtained from the deposited clone at the 107<sup>th</sup> codon. More particularly, the 107<sup>th</sup> codon of the nucleotide sequence in original Figures 1A-1D shows an AAC, encoding for an Asn, which differs from the TAC sequence, encoding for a Tyr, deduced from the DNA clone contained in ATCC Deposit Number 97334.

7. The differences in the nucleotide and encoded amino acid sequences noted in paragraphs 5-6 above have been adjusted in the version of Figures 1A-1D attached hereto as Exhibit F. Exhibit G is a marked up version of original Figures 1A-1D showing in red ink the changes made. The nucleotide sequence shown in Exhibit G is identical at

all but one nucleotide to that shown in original Figures 1A-1D; the amino acid sequence shown in Exhibit F is identical at all but one amino acid residue to that shown in original Figures 1A-1D, with the same start codon, stop codon, and length.

8. Based on the experiments described above and the high degree of similarity between the nucleotide and amino acid sequences of original Figures 1A-1D and the corresponding sequences of the deposited clone as shown in Exhibits E, it is my belief that a person of ordinary skill in the art, upon routine sequencing of the DNA clone contained in the DNA plasmid of ATCC Deposit Number 97334 using methods well known in the art prior to January 11, 1996, would readily determine that the residue at position 491 is an A residue; and thus, the encoded amino acid at position 107 is Tyr, especially when using original Figures 1A-1D as a guide.

9. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date:

3/14/02

Melanie Lenhart  
Melanie Lenhart